STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/512,045_

Source: _PCT/10_

Date Processed by STIC: _8/22/05_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.2.2 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , **EFS Submission User Manual** - ePAVE)
2. **U.S. Postal Service:** Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):** U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building. 401 Dulany Street. Alexandria, VA 22314
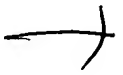
Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/512,045_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____Wrapped Nucleics Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to 3; this will prevent "wrapping."

2 ____Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____Misaligned Amino Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 ____Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**

5 ____Variable Length — Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____PatentIn 2.0 "bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7 ____Skipped Sequences (OLD RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences

8 ____Skipped Sequences (NEW RULES) — Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence
<210> sequence id number
<400> sequence id number
000

9 ____Use of n's or Xaa's (NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____Invalid <213> Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 ____Use of <220> — Sequence(s)_____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12 ____PatentIn 2.0 "bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

PCT

RAW SEQUENCE LISTING   DATE: 08/22/2005
PATENT APPLICATION: US/10/512,045   TIME: 16:49:53

Input Set : A:\P70201US0 sequence listing.txt
Output Set: N:\CRF4\08222005\J512045.raw

```
    3 <110> APPLICANT: NEOVACS
    5 <120> TITLE OF INVENTION: non immunosuppressive immunogenic or vaccine
    6       composition comprising a mutated E7 protein
    7       of the HPV-16 virus
    9 <130> FILE REFERENCE: NEOVACS - N729-PCT
C-->11 <140> CURRENT APPLICATION NUMBER: US/10/512,045
C-->12 <141> CURRENT FILING DATE: 2004-10-21
   14 <150> PRIOR APPLICATION NUMBER: FR0205173
   15 <151> PRIOR FILING DATE: 2002-04-24
   17 <160> NUMBER OF SEQ ID NOS: 4
   19 <170> SOFTWARE: PatentIn Ver. 2.1
```

ERRORED SEQUENCES

```
      51 <210> SEQ ID NO: 2
      52 <211> LENGTH: 276
E-->  53 <212> TYPE: ADN
      54 <213> ORGANISM: artificial sequence
      56 <220> FEATURE:
      57 <223> OTHER INFORMATION: artificial sequence
      58       description : E7-delta-21-26
      60 <400> SEQUENCE: 2
      61 catggagata cacctacatt gcatgaatat atgttagatt tgcaaccaga gacaactcaa 60
      62 ttaaatgaca gctcagagga ggaggatgaa atagatggtc cagctggaca agcagaaccg 120
      63 gacagagccc attacaatat tgtaaccttt tgttgcaagt gtgactctac gcttcggttg 180
      64 tgcgtacaaa gcacacacgt agacattcgt actttggaag acctgttaat gggcacacta 240
      65 ggaattgtgt gccccatctg ttctcagaaa ccataa                            276
      97 <210> SEQ ID NO: 4
      98 <211> LENGTH: 294
E-->  99 <212> TYPE: ADN
     100 <213> ORGANISM: Human papillomavirus type 16
     102 <400> SEQUENCE: 4
     103 catggagata cacctacatt gcatgaatat atgttagatt tgcaaccaga gacaactgat 60
     104 ctctactgtt atgagcaatt aaatgacagc tcagaggagg aggatgaaat agatggtcca 120
     105 gctggacaag cagaaccgga cagagcccat tacaatattg taaccttttg ttgcaagtgt 180
     106 gactctacgc ttcggttgtg cgtacaaagc acacgtag acattcgtac tttggaagac 240
     107 ctgttaatgg gcacactagg aattgtgtgc cccatctgtt ctcagaaacc ataa         294
```

Handwritten annotations:
invalid. Do you mean "DNA"?
Does Not Comply, Corrected Diskette Needed
give source of genetic material (see item 11 on Error Summary Sheet)
same error
same error in Sequence 1

Input Set : **A:\P70201US0 sequence listing.txt**
Output Set: **N:\CRF4\08222005\J512045.raw** .

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:53 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:2
L:99 M:310 E: (3) Wrong or Missing Sequence Type, numeric identifier <212>, for SEQ ID#:4